

## SEQUENCE PROTOCOL

&lt;110&gt; Degussa AG

5 &lt;120&gt; Nucleotide sequences which code for the sigE gene

&lt;130&gt; 000445 BT

&lt;140&gt;

10 &lt;141&gt;

&lt;160&gt; 8

15 &lt;170&gt; Patent In Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1330

&lt;212&gt; DNA

20 &lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (302)..(949)

25 &lt;223&gt; sigE gene

&lt;400&gt; 1

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 ttatagtcta gagcgcgagcag ggcgagatgtg aagtacctac acgcattaag tgcaaatgaa 240  
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 a atg act tat atg aaa aag aag tcc cga gat gac gca ccc gtc gta atc 349  
 Met Thr Tyr Met Lys Lys Lys Ser Arg Asp Asp Ala Pro Val Val Ile  
 1 5 10 15

gaa acc gtt caa gca gaa cat gct gaa gaa ctc acg ggc act gca gca 397  
 Glu Thr Val Gln Ala Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala  
 20 25 30

ttc gat gct gga cag gca gac atg cca aca tgg ggc gag cta gtc gca 445  
 Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala  
 35 40 45

gaa cat gca gat agc gtt tac cgc ctc gcg tac cgt ctt tcc ggc aac 493  
 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn  
 50 55 60

cag cac gat gct gaa gac ctg acc caa gaa aca ttc atg cgt gtc ttc 541  
 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe  
 55 65 70 75 80

cgc tcg ttg aag agc tac cag cca ggc acc ttt gag ggc tgg ctg cac 589  
 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His  
 85 90 95

Sub A1

5 cgc atc acc acc aac ttg ttc ctt gat atg gtt cgc cac cgc ggc aag 637  
 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys  
 100 105 110  
 atc cgc atg gag gcg ctg cct gaa gat tat gag cgc gtt ccg ggc aat 685  
 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn  
 115 120 125  
 10 gac atc acc cca gag cag gca tac acc gaa gct aac ctt gac cca gct 733  
 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala  
 130 135 140  
 15 ctg cag gca gcc ctc gat gag ttg agc cca gac ttc cgc gtg gca gtg 781  
 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val  
 145 150 155 160  
 20 atc ctc tgt gat gtt gtt ggt atg agc tat gac gaa atc gca gag acc 829  
 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr  
 165 170 175  
 ctc gga gtg aaa atg ggt acc gtg cgt tcc cgt att cac cgt gga cgc 877  
 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg  
 180 185 190  
 25 agc cag ctt cgt gca agt ttg gaa gct gca gca atg acc agc gag gaa 925  
 Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu  
 195 200 205  
 30 gtt tct ttg ttg gtt cca acc cac taaagttggt gtgttttctg acacgacaaa 979  
 Val Ser Leu Leu Val Pro Thr His  
 210 215  
 35 cgcaaagtgc gtgtcatttt tgcagctcag tgcattattt tggggttcgt ggtgcggaca 1039  
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 40 ccgcgaatct ccaagctaaa agtcgagatc gtcaggatc taaagcaaag cgcagcaggc 1219  
 caagttttga ttcagtagcg cgggatgttt tggatgttcg aacaaaaaca gcacaagtta 1279  
 45 aaaacaaggc taaagagttt tctctgttg atcacotttc agcagacgcc g 1330  
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 20 25 30

Sub A1

5 Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala  
 35 40 45  
 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn  
 50 55 60  
 10 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe  
 65 70 75 80  
 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His  
 85 90 95  
 15 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys  
 100 105 110  
 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn  
 115 120 125  
 20 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala  
 130 135 140  
 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val  
 145 150 155 160  
 25 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr  
 165 170 175  
 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg  
 180 185 190  
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 35 Val Ser Leu Leu Val Pro Thr His  
 210 215  
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 45 <220>  
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 gtacgcggct gggggaatag ccggcctcgc ggaagagtgc tttggcctgg cgctgatgct 360  
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<210> 4  
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&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

5 &lt;223&gt; downstream region

&lt;400&gt; 4

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 ttgtgcactg cgctgaatgt agggaaagaga ttaaccgtca gcgggaaacc gttgattatc 120  
 tccgctcaga gtgcaaaaac gaagaagtgt ccgcccgaat ggacctcaaa gcacggcttg 180  
 ccagcctcgc cactgagtgc atgcctggcc ctggcgcgaga gaatttagca atgcagcgcc 240  
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15 &lt;210&gt; 5

&lt;211&gt; 2086

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

20 &lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (759)..(1406)

&lt;223&gt; sigE

25 &lt;400&gt; 5

tagtcaccac ggtaagcct gcaccaaggg gcaggcgagc aacgtgtgcy ccttcaatgg 60

aacgaatata ttcacggcg tcacgtgctg cttgggtgtc acgatccttg cgggtttgat 120

30 ccgcaatggt gccgtcaagg agcgcatcgg cgagcaccag cgcaccgcct cgtcgaagaa 180

gcggccaggc ggcgtcgaca agcgcttcta aatccatggg ggagacttgg ccgaagacaa 240

gctgatagct gtcgttgga aggcgaactca tcacgtcgag cgggcgcgag agcaagaagc 300

35 gtacgcggct gggggaatag ccggcctcgc ggaagagtgc tttggcctgg cgctgatgct 360

ctgattcagg atcaatgcag gtcagtgtgg tgttatcggc cagtccgttc aggatataca 420

40 gaccaccaa cccggcagcc ggggtaatcg cgatggcacc agtggagccg ttgccattgg 480

tggtggcagc caaagtgggt agcagctggc cagtcatttc atccggggcg gggagaccga 540

45 actcggcggc gtcttcacga gcgcgcgcta cagcagcgtc ggtttcagta gtggactcga 600

cataagtgcg aagatactcg aaggcgttac tcacgcgtta tagtctagag cgagcaggcg 660

agatgtgaag tacctacag cattaagtgc aaatgaattc acaattgcca gaagatgcac 720

50 aggatgtaat ctagatttcc caagttcagt ggggcaaa atg act tat atg aaa aag 776

Met Thr Tyr Met Lys Lys

1

5

55 aag tcc cga gat gac gca ccc gtc gta atc gaa acc gtt caa gca gaa 824

Lys Ser Arg Asp Asp Ala Pro Val Ile Glu Thr Val Gln Ala Glu

10

15

20

Sub A1

	cat gct gaa gaa ctc acg ggc act gca gca ttc gat gct gga cag gca	872
	His Ala Glu Glu Leu Thr Gly Thr Ala Ala Phe Asp Ala Gly Gln Ala	
	25 30 35	
5	gac atg cca aca tgg ggc gag cta gtc gca gaa cat gca gat agc gtt	920
	Asp Met Pro Thr Trp Gly Glu Leu Val Ala Glu His Ala Asp Ser Val	
	40 45 50	
10	tac cgc ctc gcg tac cgt ctt tcc ggc aac cag cac gat gct gaa gac	968
	Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn Gln His Asp Ala Glu Asp	
	55 60 65 70	
15	ctg acc caa gaa aca ttc atg cgt gtc ttc cgc tcg ttg aag agc tac	1016
	Leu Thr Gln Glu Thr Phe Met Arg Val Phe Arg Ser Leu Lys Ser Tyr	
	75 80 85	
20	cag cca ggc acc ttt gag ggc tgg ctg cac cgc atc acc acc aac ttg	1064
	Gln Pro Gly Thr Phe Glu Gly Trp Leu His Arg Ile Thr Thr Asn Leu	
	90 95 100	
25	ttc ctt gat atg gtt cgc cac cgc ggc aag atc cgc atg gag gcg ctg	1112
	Phe Leu Asp Met Val Arg His Arg Gly Lys Ile Arg Met Glu Ala Leu	
	105 110 115	
30	cct gaa gat tat gag cgc gtt ccg ggc aat gac atc acc cca gag cag	1160
	Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn Asp Ile Thr Pro Glu Gln	
	120 125 130	
35	gca tac acc gaa gct aac ctt gac cca gct ctg cag gca gcc ctc gat	1208
	Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala Leu Gln Ala Ala Leu Asp	
	135 140 145 150	
40	gag ttg agc cca gac ttc cgc gtg gca gtg atc ctc tgt gat gtt gtt	1256
	Glu Leu Ser Pro Asp Phe Arg Val Ala Val Ile Leu Cys Asp Val Val	
	155 160 165	
45	ggt atg agc tat gac gaa atc gca gag acc ctc gga gtg aaa atg ggt	1304
	Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr Leu Gly Val Lys Met Gly	
	170 175 180	
50	acc gtg cgt tcc cgt att cac cgt gga cgc agc cag ctt cgt gca agt	1352
	Thr Val Arg Ser Arg Ile His Arg Gly Arg Ser Gln Leu Arg Ala Ser	
	185 190 195	
55	ttg gaa gct gca gca atg acc agc gag gaa gtt tct ttg ttg gtt cca	1400
	Leu Glu Ala Ala Ala Met Thr Ser Glu Glu Val Ser Leu Leu Val Pro	
	200 205 210	
60	acc cac taaagttggt gtgttttctg acacgacaaa cgaaaatgtc gtgtcatttt	1456
	Thr His	
	215	
65	tgcagctcag tgcattattt tggggttcgt ggtgcggaca ggaacttat cacaggcgac	1516
70	atccgttttg agtagtaggt atcttgata agaagttacc cacatccttg aaagtcgaga	1576
75	cacaggaggt catcggaaga tatgttcaat tccgacacca ccgcaatct ccaagctaaa	1636
80	agtcgagatc gtgcaggatc taaagcaaag cgcagcaggc caagttttga ttcagtagcg	1696

Sub A1

5 cgggatgttt tggatgttcg aacaaaaaca gcacaagtta aaaacaaggc taaagagttt 1756  
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 10 attaacgctc agcgggaaac cgttgattat ctccgctcag agtgcaaaaa cgaagaagtg 1936  
 tccgccccaa tggacctcaa agcacggctt gccagcctcg cactgagtg catgcctggc 1996  
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&lt;210&gt; 6

&lt;211&gt; 216

&lt;212&gt; PRT

20 &lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 6

Met Thr Tyr Met Lys Lys Lys Ser Arg Asp Asp Ala Pro Val Val Ile  
 1 5 10 15  
 25 Glu Thr Val Gln Ala Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala  
 20 25 30  
 30 Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala  
 35 40 45  
 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn  
 50 55 60  
 35 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe  
 65 70 75 80  
 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His  
 85 90 95  
 40 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys  
 100 105 110  
 45 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn  
 115 120 125  
 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala  
 130 135 140  
 50 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val  
 145 150 155 160  
 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr  
 165 170 175  
 55 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg  
 180 185 190

Sub A1

Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu  
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Val Ser Leu Leu Val Pro Thr His  
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5  
10  
15  
20  
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000445 BT / IS AL